

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application.

Listing of Claims:

1. (Previously presented) An isolated polynucleotide sequence comprising SEQ ID NO: 113 comprising a functional vascular tissue-specific *E. grandis* cOMT promoter.

2. (Currently amended) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

SEQ ID NO: 12, SEQ ID NO: 60, nucleotides 1-1643 of SEQ ID NO: 113, nucleotides 1019-1643 of SEQ ID NO: 113; ~~nucleotides 1525-1643 of SEQ ID NO: 113 and fragments thereof their complements, wherein said sequence and said fragments thereof comprise~~ comprises a functional vascular tissue-specific *E. grandis* cOMT promoter.

3. (Previously presented) A genetic construct comprising a polynucleotide sequence of claim 1 or claim 2.

4. (Previously presented) A genetic construct comprising, in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a DNA sequence of interest; and
- (c) a gene termination sequence,

wherein the promoter sequence comprises a polynucleotide sequence of claim 1 or claim 2; wherein said promoter sequence possesses vascular tissue-specific promoter function of the *E.grandis* cOMT gene.

5. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest is operably linked to the promoter in an antisense orientation.

6. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest is a coding

sequence operably linked to the promoter in a sense orientation.

7. (Currently amended) The genetic construct of claim 4, wherein the DNA sequence of interest is a RNAi expression construct encoding sequence present in sense and antisense orientations in the construct.

8. (Original) The genetic construct of claim 4, wherein the DNA sequence of interest comprises a non-coding sequence operably linked to the promoter in a sense orientation.

9. (Previously presented) A genetic construct comprising in the 5'-3' direction:

- (a) a promoter sequence;
- (b) a polynucleotide sequence of claim 1 or 2; and
- (c) a gene termination sequence,

wherein the promoter sequence in (a) comprises a xylem-specific promoter sequence that is different from the polynucleotide sequence of (b).

10. (Previously presented) A host cell comprising the genetic construct of claims 4, 8 or 9.

11. (Previously presented) The host cell of claim 10, wherein the host cell is a plant cell.

Claims 12-14. (Cancelled).

15. (Currently amended) A method for identifying a gene responsible for a desired function or phenotype, comprising:

- (a) transforming a plant cell with the a genetic construct of claim 4, wherein said DNA sequence of interest comprises said gene comprising a polynucleotide sequence of claim 1 or 2;
- (b) cultivating the plant cell under conditions conducive to regeneration and mature plant growth to provide a transgenic plant in which is gene is expressed; and

(c) comparing the phenotype of the transgenic plant with the phenotype of a non-transformed plant, wherein said transgenic plant possesses the desired phenotype resulting from a change in lignification as compared to said non-transformed plant; and

~~wherein the gene encodes a polypeptide involved in secondary cell wall formation.~~

16. (Previously presented) The method of claim 15, wherein said lignification is reduced in said transgenic plant as compared to said non-transformed plant.

17. (Previously presented) The genetic construct of claim 9, wherein said polynucleotide sequence of (b) is inserted in said construct as a direct or inverted repeat.

18. (Currently amended) An isolated polynucleotide sequence comprising a sequence selected from the group consisting of:

a polynucleotide comprising a 20-mer, a 40-mer, a 60-mer, an 80-mer, a 100-mer, a 120-mer, a 150-mer, a 180-mer, a 220-mer, a 250-mer, a 300-mer, 400-mer, 500-mer or 600-mer of a sequence recited in SEQ ID NO: 12 or SEQ ID NO: 113, claim 1 or claim 2.

19. (New) The isolated polynucleotide sequence of claim 2, wherein said fragments thereof comprise nucleotides 1525-1643 of SEQ ID NO: 113.

20. (New) The method of claim 15, wherein said DNA sequence of interest encodes a polypeptide involved in xylogenesis.

21. (New) The isolated polynucleotide sequence of claim 18, wherein said sequence recited in SEQ ID NO: 113 is selected from the group consisting of SEQ ID NO: 60, nucleotides 1-1643 of SEQ ID NO: 113, nucleotides 1019-1643 of SEQ ID NO: 113; and nucleotides 1525-1643 of SEQ ID NO: 113.